Amendments to the Specification

Please replace paragraph "Figure 1" on page 6, with the following amended paragraph:

FIGURE 1 shows the sequence similarity between several members of the RENT family of highly repetitive sequences. **Figure 1(A)** shows a graphic representation of the sequence alignments between the different RENT clones and T1275. **Figure 1(B)** shows deletion and insertion constructs of the 5' untranslated leader region of T1275 regulatory element and construction of transformation vectors. The constructs are presented relative to T1275-GUS-nos or 35S-GUS-nos. The arrow indicates the transcriptional start site. Plant DNA is indicated by the solid line labeled T1275, the 35S regulatory region by the solid line labelled CaMV35S, the *NdeI* - *SmaI* ("N") region by a filled in box, the shaded box coding for the amino terminal peptide, and the promoterless GUS-*nos* gene is indicated by an open box. The deletion construct removing the *NdeI* - *SmaI* fragment of T1275-GUS-nos is identified as T1275-N-GUS-nos. The *NdeI* - *SmaI* fragment from T1275-GUS-nos was also introduced into 35S-GUS-nos to produce 35S+N-Gus-nos. **Figure 1 (C)** shows the actual sequence alignments of Figure 1 (A). tCUP (nucleotides SEQ ID NO:33), Rent 1 (SEQ ID NO:10), Rent 2 (SEQ ID NO:11), Rent 3 (SEQ ID NO:12), Rent 5 (SEQ ID NO:13), and Rent 7 (SEQ ID NO:14).

Please replace paragraph "Figure 6" on pages 8-10, with the following amended paragraph:

FIGURE 6 shows several fragments, analogs and derivatives of dNm (also referred to as $*N^M$), and their associated activities in a yeast expression system. **Figure 6(A)** shows a graphic representation of 5 fragments of dNm, L1-L5 (Linker1 to Linker 5, respeectively). **Figure 6(B)** shows the nucleotide sequences of L1-L5 (Linker 1 to Linker 5; SEQ ID NO's: 5-9, respectively). **Figure 6(C)** shows the activity of constructs comprising the linkers of Figure 6(B) within a yeast expression system. pYEGUS, pYES2 with GUS and no added translational regulatory element; pYENGUS, pYES2 with the *NdeI-SmaI* fragment ("N") of tCUP and GUS; pYEL1GUS to pYEL5GUS, pYES2 with each of Linker1 to Linker 5 and GUS, respectively. **Figure 6(D)** shows the nucleotide sequences (corresponding to the RNA sequences) of L2 (linker2 SEQ ID NO: 6), L2C (nucleotides 1-16 of SEQ ID NO:6), and L2R (nucleotides 10-24 of SEQ ID NO:6). **Figure 6(E)** shows the activity of constructs comprising either the inducible promoter P_{gal1} or the constitutive promoter P_{ADH1}, in operative association with "N", L2, L2C and L2R within a yeast

expression system. pYEGUS, pYENGUS, as defined above; pYEL2GUS, pYES2 with L2 and GUS; pYEL2CGUS, pYES2 with L2C and GUS; pYEL2RGUS, pYES2 with L2R and GUS. pADHGUS: pYES2 comprising the P_{ADH1} promoter and GUS; pADHL2GUS, pADHL2CGUS, and pADHL2RGUS, each consisting of pADHGUS along with L2, L2C and L2R fragment, respectively, and in operative association with GUS. **Figure 6(F)** shows the nucleotide sequence of L2 SEQ ID NO:6), and several analogs of L2, (SCAN1-SCAN to 7, SEQ ID NO"s: 15-21, respectively) comprising different triplet base changes (in bold) of L2. **Figure 6(G)** shows the activity of constructs comprising "N", L2, L2C, L2R, and SCAN1 to SCAN7 within a yeast expression system. pYEGUS, pYENGUS, pYEL2GUS, pYEL2CGUS, pYEL2RGUS, as defined above; pYESCAN1GUS to pYESCAN7GUS, pYES2 with each of SCAN1 to SCAN7, respectively, and GUS. **Figure 6(H)** shows the activity of constructs comprising the yeast constitutive P_{ADH1} promoter, in the absence (pADHGUS) and presence (pADHL2GUS) of L2, within a yeast expression system. **Figure 6 (I)** shows a graphic representation and nucleotide sequence of the fragments derived from dN^m which have been tested in yeast. Constructs pYEL1GUS – pYEL5GUS include L1 –L5 (SEQ ID NO's:5-9), respectively; Constructs pYEL2CGUS, pYEL2RGUS and pYELMGUS include L2C, L2R and LM (nucleotides 1-16 of SEQ ID NO:6, nucleotides 10-24 of SEQ ID NO:6, and nucleotides 10-17 of SEQ ID NO:6), respectively; Constructs pYESCAN1GUS– pYESCAN7GUS include SCAN1-SCAN7 (SEQ ID NO's:15-21), respectively; Construct pYEB1-L2GUS includes B1-L2 (SEQ ID NO:23); Construct pYEB7-L2GUS includes B7-L2 (SEQ ID NO:24); Construct pYEL2D1GUS includes L2D1 (SEQ ID NO:25); Construct pYEL2D2GUS includes L2D2 (SEQ ID NO:26); Construct pYEL2D3GUS includes L2D3 (SEQ ID NO:27); and Construct pYE2L2GUS includes 2L2 (SEQ ID NO:22). **Figure 6 (J)** shows the activity within a yeast expression system of the constructs comprising deletions of the motifs AAA and ACC within L2, as shown in Figure 6 (I). pYEGUS, pYEL2GUS, pYESCAN3GUS and pYESCAN7GUS, as defined above; pYEL2D1GUS, pYES2 with L2D1 and GUS; pYEL2D2GUS, pYES2 with L2D2 and GUS; pYEL2D3GUS, pYES2 with L2D3 and GUS. **Figure 6 (K)** shows the activity within a yeast expression system of the constructs comprising L2 homologues from the RENT family, as shown in Figure 6 (I). pYEGUS, pYEL2GUS, as defined above; pYEB1L2GUS, pYES2 with B1-L2 and GUS; pYEB7L2GUS, pYES2 with B7-L2 and GUS. **Figure 6 (L)** shows the activity within a yeast expression system of the construct comprising a duplicated version of L2, as shown in Figure 6 (I). pYEGUS, pYEL2GUS, as defined above; pYE2L2GUS, pYES2 with 2xL2 and GUS. **Figure 6 (M)** shows the graphic representation and nucleotide sequence of constructs using the ADH1 promoter and tested in the yeast system (see Figure 6 (H)). Construct pADHL2GUS includes L2

(SEQ ID NO:6) **Figure 6 (N)** shows the graphic representation and nucleotide sequence of constructs where the position of L2 was varied in relation to the predicted start of transcription. The sequence between the start of transcription and L2 is shown (pYEl2GUS SEQ ID NO:28; pYE330L2GUS, SEQ ID NO:29; pYE373L2GUS, SEQ ID NO:30; pYE349L2GUS, SEQ ID NO:31; pYE400L2GUS, SEQ ID NO:32). **Figure 6 (O)** shows the activity within a yeast expression system of the constructs where L2 is located at varying position relative to the predicted transcription start, as shown in Figure 6 (N). GUS, N, dN^m , L2, L3 and L4 are pYEGUS, pYENGUS, $pYEdN^mGUS$, and pYEL2GUS, pYEL3GUS, pYEL4GUS, as defined above; 330, pYES2 with 6 bases in front of the CAP site and prior to linker 2; 373, pYES2 with 25 bases in front of the CAP site and prior to linker 2; 349, pYES2 with 49 bases in front of the CAP site and prior to linker 2; 400, pYES2 with 76 bases in front of the CAP site and prior to linker 2. **Figure 6 (P)** shows the stability of the GUS mRNA from pYEGUS and pYEL2GUS in the yeast expression system. Figure 6(P).1 shows a Northern blot analysis of culture sampled at various time points after repression of the GAL1 promoter. The Northern was probed with a GUS cDNA probe. Figure 6(P).2 shows the mean value of three experiments as the one shown in Figure 6(P).1. The Northern results were quantified and normalised for rRNA content. For each experiment, the amount of GUS RNA present in time=0 samples was arbitrarily attributed the value of 100 and RNA at other time points were calculated in relation to this value.

Please replace paragraph "Figure 7" on pages 10-11, with the following amended paragraph:

FIGURE 7 shows the relative activity of several constructs within a variety of plant systems. **Figure 7(A)** shows a graphic representation and nucleotide sequence of several fragments and derivatives of dN^m in association with the promoter EntCUP2 (also referred to as tCUP2; constructs pUCtCUP2L1GUS–pUCtCUP2L5GUS include L1-L5, SEQ ID NO's: 5-9, respectively; constructs pUCtCUP2SCN3GUS and pUCtCUP2SCAN7GUS include SCAN 3 and SCAN 7, SEQ ID NO's:17 and 21, respectively; construct pUCtCUP2-2L2GUS includes 2L2, SEQ ID NO:22). **Figure 7(B)** shows the relative activity of several constructs within a tobacco transient assay using leaf disks of uniform size. The activity of the constructs in the leaf disks are expressed as pmoles MU/min/mg GUS protein. L1, L2, L3, L4 and L5 comprise enhanced tCUP2 regulatory element linked with L1 (tCUP2-L1-GUS-nos), L2 (tCUP2-L2-GUS-nos), L3 (tCUP2-L3-GUS-nos), L4 (tCUP2-L4-GUS-nos), or L5 (tCUP2-L5-GUS-nos) respectively; "EntCUP2" (also referred to as tCUP2) comprises tCUP2-GUS-nos; "-N" comprises tCUP2 with the N fragment removed (tCUP2 (-N)). **Figure 7(C)** shows the relative activity of several constructs within an alfalfa

transient assay using a cell suspension culture. The activity of the constructs in the bombarded cell layer is expressed as the number of blue foci per plate. tCUP-L1 to L5 comprise enhanced tCUP2 regulatory element linked with L1 (tCUP2-L1-GUS-nos), L2 (tCUP2-L2-GUS-nos), L3 (tCUP2-L3-GUS-nos), L4 (tCUP2-L4-GUS-nos), or L5 (tCUP2-L5-GUS-nos) respectively; tCUP2 (also referred to as entCUP2) comprises tCUP2-GUS-nos; tCUP2-N comprises tCUP2 with the N fragment removed (tCUP2 (-N)). **Figure 7(D)** shows the evaluation of the expression of tCUP leader elements with the enhanced tCUP2 regulatory element in a transient GUS gene expression system in white spruce callus. Activity is expressed as the number of blue foci per plate. tCUP2-L1, tCUP2-L2, tCUP2-L3, tCUP2-L4 and tCUP2-L5 comprise enhanced tCUP2 regulatory element linked with L1 (tCUP2-L1-GUS-nos), L2 (tCUP2-L2-GUS-nos), L3 (tCUP2-L3-GUS-nos), L4 (tCUP2-L4-GUS-nos), or L5 (tCUP2-L5-GUS-nos) respectively; tCUP2 (also refered to as EntCUP2 or EnhtCUP2) comprises tCUP2-GUS-nos; tCUP2-N (also referred to as -N) comprises tCUP2 with the N fragment removed (tCUP2 (-N)).

Please replace paragraph "Figure 8" on pages 11-12, with the following amended paragraph:

FIGURE 8 shows the activity of constructs within a range of different plants. **Figure 8(A)** shows the constructs used for the studies presented in Figures 8 (B)-(D) pertaining to *Nde*I-*Sma*I fragment (N) and derivatives of the 35S sequence. Constructs pUC35Sl2GUS and pUC35SL4GUS include L2 and L4, SEQ ID NO's: 6 and 8, respectively. **Figure 8(B)** shows GUS activity of several constructs within a stable *Arabidopsis* transformation system, expressed as pmoles MU/min/mg GUS protein ("n" corresponds to sample size). "L2" and "L4": 35S linked with L2 and GUS (35S-L2-GUS-nos), or L4 and GUS (35S-L4-GUS-nos), respectively; "Delta*" (also referred to as $35SdN^m$) comprises 35S linked with dN^m and GUS; "GUS" comprises 35S linked directly to GUS (35S-GUS-nos). **Figure 8(C)** shows the relative activity of several constructs within a pea protoplast expression system. The activity of the constructs in the protoplasts are expressed as a ratio of GUS to luciferase (control) activity. 35SL2 and 35SL4 comprises 35S linked with L2 and GUS (35S-L2-GUS-nos), or L4 and GUS (35S-L4-GUS-nos), respectively; 35S+N comprises 35S linked with the *Nde*I-*Sma*I fragment (35S+N-GUS-nos); 35S comprises linked with GUS (35S-GUS-nos). **Figure 8(D)** shows the relative activity of several constructs within a tobacco transient assay using leaf disks of uniform size. The activity of the constructs in the leaf disks are expressed as pmoles MU/min/mg GUS protein. 35SL2 and 35SL4 comprises 35S linked with L2 and GUS (35S-L2-GUS-nos), or L4 and GUS (35S-L4-GUS-nos), respectively; "35S+N" comprises 35S linked with the *Nde*I-*Sma*I fragment and GUS (35S+N-GUS-nos); 35S

comprises 35s linked with (GUS35S-GUS-nos). **Figure 8 (E)** shows the relative activity of constructs within an alfalfa transient assay using a cell suspension culture. The activity of the constructs in the bombarded cell layer is expressed as the number of blue foci per plate. 35SL2 and 35SL4 comprises 35S linked with L2 and GUS (35S-L2-GUS-nos), or L4 and GUS (35S-L4-GUS-nos), respectively; 35SdN^{m} comprises 35S linked with dN^{m} (35SdN^{m}-GUS- nos); 35S comprises 35S linked directly to GUS (35S-GUS-nos). **Figure 8 (F)** shows the relative activity of constructs within a corn transient assay using a callus culture derived from maize embryos. Activity is expressed as the number of blue foci per plate (n is the number of plates counted). Asterisks above the graph bars indicate the intensity of the foci. Calli were submitted to an overnight histological staining assay, two days after bombardment. 35SL2 and 35SL4 comprises 35S linked with L2 and GUS (35S-L2-GUS-nos), or L4 and GUS (35S-L4-GUS-nos), respectively; 35Sdelta* comprises 35S linked with the dN^{m} (35SdN^{m}-GUS- nos); 35S comprises 35S linked directly to GUS (35S-GUS-nos). **Figure 8 (G)** shows the relative activity of tCUP leader elements in a transient expression system in white spruce callus. Activity is expressed as the number of blue foci per plate. 35SL2 and 35SL4 comprises 35S linked with L2 (35S-L2-GUS-nos), or L4 (35S-L4-GUS-nos), respectively; 35SdN ^{m} (also referred to as 35S**) comprises 35S linked with dN^{m} which is derived from tCUPdN but lacks the Kozak consensus sequence and the N terminal peptide; 35S comprises 35S-GUS-nos.

Please replace paragraph "Figure 9" on pages 12-14, with the following amended paragraph:

FIGURE 9 shows several fragments, analogs and derivatives of dN^{m}, and their associated activities in a range of plant species and in conifers. **Figure 9 (A)** shows a graphic representation and nucleotide sequence of fragments and derivatives of dN^{m} in association with the promoter EntCUP3 (also referred to as tCUP3). Constructs pUCtCUP3L2GUS and pUCtCUP3-2XI2GUS include L2 and 2L2 (SEQ ID NO's:6 and 22), respectively. **Figure 9 (B)** shows the relative activity of several constructs within a tobacco transient assay using leaf disks of uniform size. The activity of the constructs in the leaf disks are expressed as pmoles MU/min/mg GUS protein. L2, Scan3 and Scan7 comprise enhanced tCUP2 regulatory element linked with L2 and GUS (tCUP2-L2-GUS-nos), Scan3 and GUS (tCUP2-Scan3-GUS-nos), Scan7 and GUS (tCUP2-Scan7-GUS-nos), respectively; "-N" comprises tCUP2 with the N fragment removed linked with GUS (tCUP2 (-N)-GUS). **Figure 9 (C)** shows GUS activity of several constructs measured in pmoles MU/min/mg within a stable *Arabidopsis* transformation system (the n corresponds to the sample size). tCUP2-L2 and tCUP2-2XL2 comprises enhanced tCUP2 regulatory element linked with L2 and

GUS (tCUP2-L2-GUS-nos), or twice the sequence of L2 and GUS (tCUP2-2XL2-GUS-nos), respectively; tCUP3-L2 and tCUP3-2XL2 comprises enhanced tCUP3 regulatory element linked with L2 and GUS (tCUP3-L2-GUS-nos), or twice the sequence of L2 and GUS (tCUP3-2XL2-GUS-nos), respectively; DNB1 comprises tCUP2-GUS-nos. **Figure 9 (D)** shows the relative activity of several constructs within a tobacco transient assay using leaf disks of uniform size. The activity of the constructs in the leaf disks are expressed as pmoles MU/min/mg GUS protein. EnhtCUP2 is also referred to as EntCUP2 and tCUP2; EnhtCUP3 is also referred to as EntCUP3 and tCUP3. EnhtCUP2-L2 and EnhtCUP2-2XL2 comprises enhanced tCUP2 regulatory element linked with L2 and GUS (tCUP2-L2-GUS-nos), or twice the sequence of L2 and GUS (tCUP2-2XL2-GUS-nos), respectively; tCUP3-L2 and tCUP3-2XL2 comprises enhanced tCUP3 regulatory element linked with L2 and GUS (tCUP3-L2-GUS-nos), or twice the sequence of L2 and GUS (tCUP3-2XL2-GUS-nos), respectively; EnhtCUP2 comprises tCUP2-GUS-nos; EnhtCUP3 comprises tCUP3-GUS-nos; EnhtCUP2(-N) comprises tCUP2 with the N fragment removed (tCUP2(-N)-GUS); EnhtCUP3(-N) comprises tCUP3 with the N fragment removed (tCUP3(-N)-GUS). Figure 9 (E) shows the evaluation of the expression of tCUP leader elements with the enhanced tCUP2 regulatory element in a transient GUS gene expression system in an alfalfa cell suspension culture. The activity of the constructs in the cell layer is expressed as the number of blue foci per plate. tCUP2-L2 and tCUP2-2xL2 comprises enhanced tCUP2 regulatory element linked with L2 and GUS (tCUP2-L2-GUS-nos), or twice the sequence of L2 and GUS (tCUP2-2xL2-GUS-nos), respectively; tCUP3-L2 and tCUP3-2xL2 comprises enhanced tCUP3 regulatory element linked with L2 and GUS (tCUP3-L2-GUS-nos), or twice the sequence of L2 and GUS (tCUP3-2xL2-GUS-nos), respectively; tCUP2 and tCUP3 comprises tCUP2-GUS-nos and tCUP3-GUS-nos respectively; tCUP2-N comprises tCUP2 with the N fragment removed (tCUP2 (-N)-GUS); tCUP3-N comprises tCUP3 with the N fragment removed (tCUP3(-N)-GUS). **Figure 9 (F)** shows an evaluation of the expression of tCUP leader elements with the enhanced tCUP2 regulatory element in a transient GUS gene expression system in white spruce callus. Activity is expressed as the number of blue foci per plate. tCUP2-L2 and tCUP2-2XL2 comprises enhanced tCUP2 regulatory element linked with L2 and GUS (tCUP2-L2-GUS-nos), or twice the sequence of L2 and GUS (tCUP2-2XL2-GUS-nos), respectively; tCUP3-L2 and tCUP3-2XL2 comprises enhanced tCUP3 regulatory element linked with L2 and GUS (tCUP3-L2-GUS-nos), or twice the sequence of L2 and GUS (tCUP3-2XL2-GUS-nos), respectively; tCUP2 and tCUP3 comprises tCUP2-GUS-nos and tCUP3-GUS-nos respectively; tCUP2-N comprises tCUP2 with the N fragment removed and GUS (tCUP2 (-N)-GUS);

tCUP3-N comprises tCUP3 with the N fragment removed and GUS (tCUP3 (-N)-GUS).

Please replace paragraph "Figure 10" on page 14, with the following amended paragraph:

FIGURE 10 shows fragments of dN^m, and their associated activities in the bacterium *Escherichia coli*. **Figure 10 (A)** shows a graphic representation and nucleotide sequence of fragments of dN^m in association with the promoter 35S. Constructs pUC35SL2GUS and pUC35SL4GUS include L2 and L4 (SEQ ID NO's:6 and8), respectively. **Figure 10 (B)** shows the relative luciferase activity of L2 and L4 in the bacterial reporter system *E. Coli*. pEPLUX comprises 35S linked to LUX, the luciferase gene. p35SL2LUX and p35SL4LUX comprises 35S linked with L2 or L4 respectively, upstream of the luciferase (LUX) ATG. –206TAP is a construct used as a negative control as it does not carry the luciferase gene.